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<!--StartFragment-->RESULT 2
ABD14347
ID   ABD14347 standard; DNA; 603 BP.
XX
AC   ABD14347;
XX
DT   29-JUL-2004 (first entry)
XX
DE   Pseudomonas aeruginosa polynucleotide #12951.
XX
KW   Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW   antibacterial.
XX
OS   Pseudomonas aeruginosa.
XX
PN   US6551795-B1.
XX
PD   22-APR-2003.
XX
PF   18-FEB-1999; 99US-00252991.
XX
PR   18-FEB-1998; 98US-0074788P.
PR   27-JUL-1998; 98US-0094190P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR   WPI; 2003-615309/58.
DR   P-PSDB; ABO80776.
XX
PT   Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT   useful as molecular targets for diagnostics, prophylaxis and treatment of
PT   pathological conditions resulting from bacterial infection.
XX
PS   Disclosure; SEQ ID NO 12951; 455pp; English.
XX
CC   The invention relates to Pseudomonas aeruginosa polypeptides and the
CC   polynucleotides encoding them. The sequences are useful in diagnosis and
CC   therapy of pathological conditions, as molecular targets for diagnostics,
CC   prophylaxis and treatment of pathological conditions resulting from a
CC   bacterial infection, for evaluating a compound, such as a polypeptide,
CC   for the ability to bind a P. aeruginosa nucleic acid, as components of
CC   effective antibacterial targets, as targets for antibacterial drugs,
CC   including anti-P. aeruginosa drugs, as templates for recombinant
CC   production of P. aeruginosa-derived peptides or polypeptides, as target
CC   components for diagnosis and/or treatment of P. aeruginosa-caused
CC   infection, and in detection of P. aeruginosa sequences or other sequences
CC   of Pseudomonas species using biochip technology. Sequences ABD01397-
CC   ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification but was obtained in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html
XX
SQ   Sequence 603 BP; 129 A; 195 C; 181 G; 98 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	2.2e-68	Length:	603
Score:	742.00	Matches:	140
Percent Similarity:	94.4%	Conservative:	12
Best Local Similarity:	87.0%	Mismatches:	9

Query Match: 90.0% Indels: 0
DB: 10 Gaps: 0

US-10-583-066-1 (1-161) x ABD14347 (1-603)

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Qy      1 MetLeuIleAlaAlaAsnLysAlaValSerIleAspTyrThrLeuThrAsnAspAlaGly 20
      |||  |||
Db      118 ATGCAGATCGCGGCCAACAAAGGCGGTTTCCATCGACTATACCCTGACCAACGACGCCGGG 177

Qy      21 GluValIleAspSerSerAlaGlyGlyAlaProLeuValTyrLeuGlnGlyAlaGlyAsn 40
      :::|
Db      178 GATGTCATCGACAGTTCCGCTGGTGGCGCGCCGCTGGTCTACCTGCACGGTGCCGGCAAC 237

Qy      41 IleIleProGlyLeuGluLysAlaLeuGluGlyLysAlaValGlyAspAspLeuGluVal 60
      |||||  |||
Db      238 ATCATCGTCGGCCTGGAGAAGGCCCTGGAAGGCAAGAACGTCGGTGACGAACCTGAGCGTC 297

Qy      61 AlaValGluProGluAspAlaTyrGlyGluTyrAlaAlaGluLeuValSerThrLeuSer 80
      |||:::|
Db      298 GCCATCGAGCCGGAAGACGCCTATGGCGAATACAGCGCCGAACCTGGTCGCGACCCTGACC 357

Qy      81 ArgSerMetPheGluGlyValAspGluLeuGluValGlyMetGlnPheHisAlaSerAla 100
      |||  |||
Db      358 CGCGAGATGTTCTGAAGGCGTCGACGAACTGGAAGTCGGCATGCAGTTCCACGCCTCGGCT 417

Qy     101 ProAspGlyGlnMetGlnIleValThrIleAlaAspLeuAspGlyAspAspValThrVal 120
      |||||  |||
Db     418 CCGGACGGCGGCATGCAGATCGTCACCATCCGCGACATCGACGGCGACGACGTGACCGTC 477

Qy     121 AspGlyAsnHisProLeuAlaGlyGlnArgLeuAsnPheLysValLysIleValAspIle 140
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Db     478 GACGGCAACCATCCGCTGGCCGGCCAGCGCCTGAACTTCAAGGTCAAGGTAGTCGACGTG 537

Qy     141 ArgAspAlaSerGlnGluGluIleAlaHisGlyHisValHisGlyGluGlyGlyHisHis 160
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Db     538 CGCGAGGCCAACGCCGAGGAAATCGCCACGGCCACATCCATGGCGAAGGCGGTACCAC 597

Qy     161 His 161
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Db     598 CAC 600
<!--EndFragment-->
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